

Table S1 Assembly metrics of the reference genome of *M. oryzae* isolate Ina168.

Features	Strain	
	Ina168	70-15
Total reads (Gb)	1.92	-
Coverage (fold)	48.4	-
Number of contigs	1,978	-
Average contigs length (kp)	20.02	-
Maximum contig length (kp)	920.1	-
N50 contig length (kb)	162.9	-
Assembly size (Mb)	39.61	41.03
A	9,676,511	9,901,089
T	9,666,293	9,915,530
G	10,120,238	10,574,756
C	10,131,235	10,558,558
N	19,978	77,800
Assembly size with A/T/G/C only (Mb)	39.59	40.95
G+C composition (%)	51.1	51.6

Contigs shorter than 500 bp were excluded.